Sequence Listing

<110> Baker, Kevin
Botstein,David
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Ferrara,Napoleone
Filvaroff,Ellen
Gerritsen,Mary
Goddard,Audrey
Godowski,Paul
Grimaldi,Christopher
Gurney,Austin
Hillan,Kenneth
Kljavin,Ivar
Napier,Mary
Roy,Margaret
Tumas,Daniel
Wood,William

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Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
             65                  70                  75

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Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
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Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
            110                 115                 120

Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
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Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
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Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
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830 835 840

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caggggggact ggtcctcctg gaggagatgc tcgccttggg gaataatcac 950

tttattggtt ttgtgaatga ttctgtgact aagtctattg tggctttgcg 1000

cttaactctg gtggtgaagg tcagcacctg tgtgccgggg gagagtcacg 1050

caaatgactt ggagtgttca ggaaaaggaa aatgcaccac gaagccgtca 1100

gaggcaactt tttcctgtac ctgtgaggag cagtacgtgg gtactttctg 1150

tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200

gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250

cttcctggtt atactggaga gctttgccag tccaagattg attactgcat 1300

cctagaccca tgcagaaatg gagcaacatg catttccagt ctcagtggat 1350

tcacctgcca gtgtccagaa ggatacttcg gatctgcttg tgaagaaaag 1400

gtggacccct gcgcctcgtc tccgtgccag aacaacggca cctgctatgt 1450

ggacggggta cactttacct gcaactgcag cccgggcttc acagggccga 1500

cctgtgccca gcttattgac ttctgtgccc tcagcccctg tgctcatggc 1550

acgtgccgca gcgtgggcac cagctacaaa tgcctctgtg atccaggtta 1600

ccatggcctc tactgtgagg aggaatataa tgagtgcctc tccgctccat 1650

gcctgaatgc agccacctgc agggacctcg ttaatggcta tgagtgtgtg 1700

tgcctggcag aatacaaagg aacacactgt gaattgtaca aggatccctg 1750

cgctaacgtc agctgtctga acggagccac ctgtgacagc gacggcctga 1800

atggcacgtg catctgtgca cccgggttta caggtgaaga gtgcgacatt 1850

gacataaatg aatgtgacag taacccctgc caccatggtg ggagctgcct 1900

ggaccagccc aatggttata actgccactg cccgcatggt tgggtgggag 1950

caaactgtga gatccacctc caatggaagt ccgggcacat ggcggagagc 2000

ctcaccaaca tgccacggca ctcctctac atcatcattg gagcctctg 2050

cgtggccttc atccttatgc tgatcatcct gatcgtgggg atttgccgca 2100

tcagccgcat tgaataccag ggttcttcca ggccagccta tgaggagttc 2150

tacaactgcc gcagcatcga cagcgagttc agcaatgcca ttgcatccat 2200

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ttctttaaaa agtcaagggt tctatattgt gagtaaatta aatttacatt 3050

tgagttgttt gttgctaaga ggtagtaaat gtaagagagt actggttcct 3100

tcagtagtga gtatttctca tagtgcagct ttatttatct ccaggatgtt 3150

tttgtggctg tatttgattg atatgtgctt cttctgattc ttgctaattt 3200

ccaaccatat tgaataaatg tgatcaagtc a 3231

<210> 15
<211> 737
<212> PRT
<213> Homo Sapien

<400> 15

Met Gln Pro Arg Arg Ala Gln Ala Pro Gly Ala Gln Leu Leu Pro
1 5 10 15

Ala Leu Ala Leu Leu Leu Leu Leu Leu Gly Ala Gly Pro Arg Gly
20 25 30

Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
35 40 45

Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60

Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
65 70 75

Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
80 85 90

Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
95 100 105

Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

110 115 120

Cys Ile Cys Asn Glu Gly Tyr Glu Gly Pro Asn Cys Glu Gln Ala
125 130 135

Leu Pro Ser Leu Pro Ala Thr Gly Trp Thr Glu Ser Met Ala Pro
140 145 150

Arg Gln Leu Gln Pro Val Pro Ala Thr Gln Glu Pro Asp Lys Ile
155 160 165

Leu Pro Arg Ser Gln Ala Thr Val Thr Leu Pro Thr Trp Gln Pro
170 175 180

Lys Thr Gly Gln Lys Val Val Glu Met Lys Trp Asp Gln Val Glu
185 190 195

Val Ile Pro Asp Ile Ala Cys Gly Asn Ala Ser Ser Asn Ser Ser
200 205 210

Ala Gly Gly Arg Leu Val Ser Phe Glu Val Pro Gln Asn Thr Ser
215 220 225

Val Lys Ile Arg Gln Asp Ala Thr Ala Ser Leu Ile Leu Leu Trp
230 235 240

Lys Val Thr Ala Thr Gly Phe Gln Gln Cys Ser Leu Ile Asp Gly
245 250 255

Arg Ser Val Thr Pro Leu Gln Ala Ser Gly Gly Leu Val Leu Leu
260 265 270

Glu Glu Met Leu Ala Leu Gly Asn Asn His Phe Ile Gly Phe Val
275 280 285

Asn Asp Ser Val Thr Lys Ser Ile Val Ala Leu Arg Leu Thr Leu
290 295 300

Val Val Lys Val Ser Thr Cys Val Pro Gly Glu Ser His Ala Asn
305 310 315

Asp Leu Glu Cys Ser Gly Lys Gly Lys Cys Thr Thr Lys Pro Ser
320 325 330

Glu Ala Thr Phe Ser Cys Thr Cys Glu Glu Gln Tyr Val Gly Thr
335 340 345

Phe Cys Glu Glu Tyr Asp Ala Cys Gln Arg Lys Pro Cys Gln Asn
350 355 360

Asn Ala Ser Cys Ile Asp Ala Asn Glu Lys Gln Asp Gly Ser Asn
365 370 375

Phe Thr Cys Val Cys Leu Pro Gly Tyr Thr Gly Glu Leu Cys Gln
380 385 390

Ser Lys Ile Asp Tyr Cys Ile Leu Asp Pro Cys Arg Asn Gly Ala
395 400 405

Thr Cys Ile Ser Ser Leu Ser Gly Phe Thr Cys Gln Cys Pro Glu
410 415 420

Gly Tyr Phe Gly Ser Ala Cys Glu Glu Lys Val Asp Pro Cys Ala
425 430 435

Ser Ser Pro Cys Gln Asn Asn Gly Thr Cys Tyr Val Asp Gly Val
440 445 450

His Phe Thr Cys Asn Cys Ser Pro Gly Phe Thr Gly Pro Thr Cys
455 460 465

Ala Gln Leu Ile Asp Phe Cys Ala Leu Ser Pro Cys Ala His Gly
470 475 480

Thr Cys Arg Ser Val Gly Thr Ser Tyr Lys Cys Leu Cys Asp Pro
485 490 495

Gly Tyr His Gly Leu Tyr Cys Glu Glu Glu Tyr Asn Glu Cys Leu
500 505 510

Ser Ala Pro Cys Leu Asn Ala Ala Thr Cys Arg Asp Leu Val Asn
515 520 525

Gly Tyr Glu Cys Val Cys Leu Ala Glu Tyr Lys Gly Thr His Cys
530 535 540

Glu Leu Tyr Lys Asp Pro Cys Ala Asn Val Ser Cys Leu Asn Gly
545 550 555

Ala Thr Cys Asp Ser Asp Gly Leu Asn Gly Thr Cys Ile Cys Ala
560 565 570

Pro Gly Phe Thr Gly Glu Glu Cys Asp Ile Asp Ile Asn Glu Cys
575 580 585

Asp Ser Asn Pro Cys His His Gly Gly Ser Cys Leu Asp Gln Pro
590 595 600

Asn Gly Tyr Asn Cys His Cys Pro His Gly Trp Val Gly Ala Asn
605 610 615

Cys Glu Ile His Leu Gln Trp Lys Ser Gly His Met Ala Glu Ser
620 625 630

Leu Thr Asn Met Pro Arg His Ser Leu Tyr Ile Ile Ile Gly Ala
635 640 645

Leu Cys Val Ala Phe Ile Leu Met Leu Ile Ile Leu Ile Val Gly
650 655 660

Ile Cys Arg Ile Ser Arg Ile Glu Tyr Gln Gly Ser Ser Arg Pro
665 670 675

Ala Tyr Glu Glu Phe Tyr Asn Cys Arg Ser Ile Asp Ser Glu Phe
680 685 690

Ser Asn Ala Ile Ala Ser Ile Arg His Ala Arg Phe Gly Lys Lys

695 700 705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
725 730 735

Asp Leu

<210> 16
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 16
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 17
caggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 18
<211> 508
<212> DNA
<213> Homo Sapien

<400> 18
ctctggaagg tcacggccac aggattccaa cagtgctccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc agggggactg gtcctcctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggtgaaggt 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttcctggtta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 19
ctctggaagg tcacggccac aggattccaa cagtgctccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc aggggactg gtcctcctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggtgaaggt 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttcctgtacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttcctggtta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
ctctggaagg tcacggccac agg 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaagc tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22
cagtgctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23
<211> 1520
<212> DNA
<213> Homo Sapien

<400> 23
gctgagtctg ctgctcctgc tgctgctgct ccagcctgta acctgtgcct 50

acaccacgcc aggcccccca agagccctca ccacgctggg cgcccccaga 100

gcccacacca tgccgggcac ctacgctccc tcgaccacac tcagtagtcc 150

cagcacccag ggcctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggtcctaag gcaggtttac 250

cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300

cagcctggac aggcttagag atggcctcgt gggcgcccag ttctggtcag 350

cctatgtgcc atgccagacc caggaccggg atgccctgcg cctcaccctg 400

gagcagattg acctcatacg ccgcatgtgt gcctcctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcatcggtgt agagggtggc cactcgctgg acaatagcct ctccatctta 550

cgtaccttct acatgctggg agtgcgctac ctgacgctca cccacacctg 600

caacacaccc tgggcagaga gctccgctaa gggcgtccac tccttctaca 650

acaacatcag cgggctgact gactttggtg agaaggtggt ggcagaaatg 700

aaccgcctgg gcatgatggt agacttatcc catgtctcag atgctgtggc 750

acggcgggcc ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800

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cagcttctga agaagaacgg tggcgtcgtg atggtgtctt tgtccatggg 900

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gattatgatg gggccggcaa attccctcag gggctggaag acgtgtccac 1050

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agcttcaggg tgtccttcgt ggaaacctgc tgcgggtctt cagacaagtg 1150

gaaaaggtac aggaagaaaa caaatggcaa agccccttgg aggacaagtt 1200

cccggatgag cagctgagca gttcctgcca ctccgacctc tcacgtctgc 1250

gtcagagaca gagtctgact tcaggccagg aactcactga gattcccata 1300

cactggacag ccaagttacc agccaagtgg tcagtctcag agtcctcccc 1350

ccacatggcc ccagtccttg cagttgtggc caccttccca gtccttattc 1400

tgtggctctg atgacccagt tagtcctgcc agatgtcact gtagcaagcc 1450

acagacaccc cacaaagttc ccctgttgtg caggcacaaa tatttcctga 1500

aataaatgtt ttggacatag 1520

<210> 24
<211> 433
<212> PRT
<213> Homo Sapien

<400> 24

Met	Pro	Gly	Thr	Tyr	Ala	Pro	Ser	Thr	Thr	Leu	Ser	Ser	Pro	Ser	
1				5				10						15	
Thr	Gln	Gly	Leu	Gln	Glu	Gln	Ala	Arg	Ala	Leu	Met	Arg	Asp	Phe	
				20				25						30	
Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Leu	Val	Leu	Arg	Gln	
				35				40						45	
Val	Tyr	Gln	Lys	Gly	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	Ser	
				50				55						60	
Tyr	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	Gly	
				65				70						75	
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg	
				80				85						90	
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg	
				95				100						105	
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys	
				110				115						120	
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu	
				125				130						135	
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe	
				140				145						150	
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn	
				155				160						165	
Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr	
				170				175						180	

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
185 190 195

Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
200 205 210

Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
215 220 225

Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
230 235 240

Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly
245 250 255

Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
260 265 270

Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
275 280 285

Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
290 295 300

Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
305 310 315

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
320 325 330

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
335 340 345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360

Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375

Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390

Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405

Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu
410 415 420

Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu
425 430

<210> 25
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggtg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatacg ccgcatgtgt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
aaaacctata aatattccgg attattcata ccgtcccacc atcgggcgcg 50

gatccgcggc cgcgaattct aaaccaacat gccgggcacc tacgctccct 100

cgaccacact cagtagtccc agcacccagg gcctgcaaga gcaggcacgg 150

gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgccct 200

ggtcctaagg caggtttacc agaaagggct acaggatgtt aacctgcgca 250

atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300

ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350

tgccctgcgc ctcaccctgg agcagattga cctcatacgc cgcatgtgtg 400

cctcctattc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450

actcagaaat tggcctgcct catcggtgta gagggtggcc actcgctgga 500

caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550

tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600

ggcgtccact ccttctacaa caacatcagc gggctgactg actttggtga 650

gaaggtggtg gcagaaatga accgcctggg catgatggta gacttatccc 700

atgtctcaga tgctgtggca cggcgggccc tggaagtgtc acaggcacct 750

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tggtgtcttt gtccatggga gtaatacagt gcaacccatc agccaatgtg 900

tccactgtgg cagatcactt cgaccacatc aaggctgtca ttggatccaa 950

gttcatcggg attggtggag attatgatgg ggccggcaaa ttccctcagg 1000

ggctggaaga cgtgtccaca tacccggtcc tgatagagga gttgctgagt 1050

cgtggctgga gtgaggaaga gcttcagggt gtccttcgtg gaaacctgct 1100

gcgggtcttc agacaagtgg aaaaggtaca ggaagaaaac aaatggcaaa 1150

gccccttgga ggacaagttc ccggatgagc agctgagcag ttcctgccac 1200

tccgacctct cacgtctgcg tcagagacag agtctgactt caggccagga 1250

actcactgag attcccatac actggacagc caagttacca gccaagtggt 1300

cagtctcaga gtcctccccc caccctgaca aaactcacac atgcccaccg 1350

tgcccagcac ctgaactcct gggggggaccg tcagtcttcc tcttcccccc 1400

aaaacccaag gacacc 1416

<210> 30
<211> 446
<212> PRT
<213> Homo Sapien

<400> 30

Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
1 5 10 15

Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30

Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45

Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

50 55 60

Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
65 70 75

Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90

Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
95 100 105

Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120

Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135

Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150

Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165

Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala
185 190 195

Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
200 205 210

Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val
215 220 225

Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg
230 235 240

Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly
245 250 255

Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro
260 265 270

Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys
275 280 285

Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp
290 295 300

Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
305 310 315

Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu
320 325 330

Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
335 340 345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
350 355 360

Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
365 370 375

Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
380 385 390

Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
395 400 405

Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
410 415 420

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
425 430 435

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
440 445

<210> 31
<211> 1790
<212> DNA
<213> Homo Sapien

<400> 31
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gcgtcccgcg ccctgcgcca ccgccgccga gccgcagccc gccgcgcgcc 100

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atccgcgcgg cggccgccgc cgttgctgcc cctgctgctg ctgctctgcg 200

tcctcggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250

ccccaggatc ccacgcttct catcggctcc tccctgctgg ccacctgctc 300

agtgcacgga gacccaccag gagccaccgc cgagggcctc tactggaccc 350

tcaacgggcg ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400

accttggctc tggccctggc caacctcaat gggtccaggc agcggtcggg 450

ggacaacctc gtgtgccacg cccgtgacgg cagcatcctg gctggctcct 500

gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550

tccaagaaca tgaaggactt gacctgccgc tggacgccag gggcccacgg 600

ggagaccttc ctccacacca actactccct caagtacaag cttaggtggt 650

atggccagga caacacatgt gaggagtacc acacagtggg gccccactcc 700

tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750

ggaggccacc aaccgcctgg gctctgcccg ctccgatgta ctcacgctgg 800

atatcctgga tgtggtgacc acggaccccc cgcccgacgt gcacgtgagc 850

cgcgtcgggg gcctggagga ccagctgagc gtgcgctggg tgtcgccacc 900

cgccctcaag gatttcctct ttcaagccaa ataccagatc cgctaccgag 950

tggaggacag tgtggactgg aaggtggtgg acgatgtgag caaccagacc 1000

tcctgccgcc tggccggcct gaaacccggc accgtgtact tcgtgcaagt 1050

gcgctgcaac ccctttggca tctatggctc caagaaagcc gggatctgga 1100

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ggcccgggcg gcggggcgtg cgaaccgcgg ggcggagagc cgagctcggg 1200

gccggtgcgg cgcgagctca agcagttcct gggctggctc aagaagcacg 1250

cgtactgctc caacctcagc ttccgcctct acgaccagtg gcgagcctgg 1300

atgcagaagt cgcacaagac ccgcaaccag gacgagggga tcctgccctc 1350

gggcagacgg ggcacggcga gaggtcctgc cagataagct gtaggggctc 1400

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gccacctctg taccctcact tcagggcacc tgagccaccc tcagcaggag 1500

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gaggccacct ttgggtgcac cccagtgggt gtgtgtgtgt gtgtgagggt 1600

tggttgagtt gcctagaacc cctgccaggg ctgggggtga gaaggggagt 1650

cattactccc cattacctag ggcccctcca aaagagtcct tttaaataaa 1700

tgagctattt aggtgctgtg attgtgaaaa aaaaaaaaaa aaaaaaaaaa 1750

aaaaaaaaaa aaaaaaaaaa aaaaacaaaa aaaaaaaaaa 1790

<210> 32
<211> 422
<212> PRT
<213> Homo Sapien

<400> 32

Met Pro Ala Gly Arg Arg Gly Pro Ala Ala Gln Ser Ala Arg Arg
1 5 10 15

Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Leu Cys Val Leu Gly
20 25 30

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
50 55 60

Ser Val His Gly Asp Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr
65 70 75

Trp Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val
80 85 90

Leu Asn Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly
95 100 105

Ser Arg Gln Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp
110 115 120

Gly Ser Ile Leu Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro
125 130 135

Glu Lys Pro Val Asn Ile Ser Cys Trp Ser Lys Asn Met Lys Asp
140 145 150

Leu Thr Cys Arg Trp Thr Pro Gly Ala His Gly Glu Thr Phe Leu
155 160 165

His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu Arg Trp Tyr Gly Gln
170 175 180

Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly Pro His Ser Cys
185 190 195

His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr Glu Ile Trp
200 205 210

Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp Val Leu
215 220 225

Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp Pro Pro Pro Asp
230 235 240

Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
245 250 255

Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala
260 265 270

Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
290 295 300

Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro
305 310 315

Phe Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp
320 325 330

Ser His Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly
335 340 345

Pro Gly Gly Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser

350 355 360

Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys
365 370 375

Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln
380 385 390

Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp
395 400 405

Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro
410 415 420

Ala Arg

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
cccgcccgac gtgcacgtga gcc 23

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 34
tgagccagcc caggaactgc ttg 23

<210> 35
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 35
caagtgcgct gcaacccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36
<211> 1771
<212> DNA
<213> Homo Sapien

<400> 36
cccacgcgtc cgctggtgtt agatcgagca accctctaaa agcagtttag 50

agtggtaaaa aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg 100

atgaaatttc ttctggacat cctcctgctt ctcccgttac tgatcgtctg 150

ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200

tcaccggcga aatcgtgctg attacaggag ctgggcatgg aattgggaga 250

ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300

tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350

gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400

tacagctctg caaagaaggt gaaggcagaa attggagatg ttagtatttt 450

agtaaataat gctggtgtag tctatacatc agatttgttt gctacacaag 500

atcctcagat tgaaaagact tttgaagtta atgtacttgc acatttctgg 550

actacaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600

tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg 650

cttactgttc aagcaagttt gctgctgttg gatttcataa aactttgaca 700

gatgaactgg ctgccttaca aataactgga gtcaaaacaa catgtctgtg 750

tcctaatttc gtaaacactg gcttcatcaa aaatccaagt acaagtttgg 800

gacccactct ggaacctgag gaagtggtaa acaggctgat gcatgggatt 850

ctgactgagc agaagatgat ttttattcca tcttctatag ctttttaac 900

aacattggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa 950

aaatcagtgt taagtttgat gcagttattg gatataaaat gaaagcgcaa 1000

taagcaccta gttttctgaa aactgattta ccaggtttag gttgatgtca 1050

tctaatagtg ccagaatttt aatgtttgaa cttctgtttt ttctaattat 1100

ccccatttct tcaatatcat ttttgaggct ttggcagtct tcatttacta 1150

ccacttgttc tttagccaaa agctgattac atatgatata aacagagaaa 1200

taccttttaga ggtgacttta aggaaaatga agaaaaagaa ccaaaatgac 1250

tttattaaaa taatttccaa gattatttgt ggctcacctg aaggctttgc 1300

aaaatttgta ccataaccgt ttatttaaca tatattttta tttttgattg 1350

cacttaaatt ttgtataatt tgtgtttctt tttctgttct acataaaatc 1400

agaaacttca agctctctaa ataaaatgaa ggactatatc tagtggtatt 1450

tcacaatgaa tatcatgaac tctcaatggg taggtttcat cctacccatt 1500

gccactctgt ttcctgagag atacctcaca ttccaatgcc aaacatttct 1550

gcacagggaa gctagaggtg gatacacgtg ttgcaagtat aaaagcatca 1600

ctgggattta aggagaattg agagaatgta cccacaaatg gcagcaataa 1650

taaatggatc acacttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1750

aaaaaaaaaa aaaaaaaaaa a 1771

<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	
1				5				10						15	
Val	Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	
				20				25						30	
Arg	Lys	Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
				35				40						45	
His	Gly	Ile	Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	
				50				55						60	
Ser	Lys	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	
				65				70						75	
Thr	Ala	Ala	Lys	Cys	Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	
				80				85						90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	
				95				100						105	
Lys	Val	Lys	Ala	Glu	Ile	Gly	Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	
				110				115						120	
Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp	Leu	Phe	Ala	Thr	Gln	Asp	Pro	
				125				130						135	
Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn	Val	Leu	Ala	His	Phe	Trp	
				140				145						150	
Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr	Lys	Asn	Asn	His	Gly	
				155				160						165	
His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His	Val	Ser	Val	Pro	
				170				175						180	
Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185				190						195	
His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile	Thr	Gly	

200 205 210

Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe
215 220 225

Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys
245 250 255

Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu
260 265 270

Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile
275 280 285

Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
ggtgaaggca gaaattggag atg 23

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
atcccatgca tcagcctgtt tacc 24

<210> 40
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 40
gctggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

<210> 41
<211> 1377
<212> DNA
<213> Homo Sapien

<400> 41
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gaaccaggac tggggtgacg gcagggcagg gggcgcctgg ccggggagaa 100

gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150

ccgaaggagg ccatcgggga gccgggaggg gggactgcga gaggaccccg 200

gcgtccgggc tcccggtgcc agcgctatga ggccactcct cgtcctgctg 250

ctcctgggcc tggcggccgg ctcgccccca ctggacgaca acaagatccc 300

cagcctctgc ccggggcacc ccggccttcc aggcacgccg ggccaccatg 350

gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400

cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgccggg 450

acctcgaggg gaccccgggc cgcgaggaga ggcgggaccc gcggggccca 500

ccgggcctgc cggggagtgc tcggtgcctc cgcgatccgc cttcagcgcc 550

aagcgctccg agagccgggt gcctccgccg tctgacgcac ccttgccctt 600

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cttcctggtc ctctgcttct ctggatcctc cccacccccc cctgctcctg 1300

gggccggccc ttttctcaga gatcactcaa taaacctaag aaccctcata 1350

aaaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
<212> PRT
<213> Homo Sapien

<400> 42

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Met Arg Pro Leu Leu Val Leu Leu Leu Leu Gly Leu Ala Ala Gly
  1               5                  10                  15

Ser Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly
             20                  25                  30

His Pro Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly
             35                  40                  45

Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly
             50                  55                  60

Ala Pro Gly Glu Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly
             65                  70                  75

Pro Arg Gly Asp Pro Gly Pro Arg Gly Glu Ala Gly Pro Ala Gly
             80                  85                  90

Pro Thr Gly Pro Ala Gly Glu Cys Ser Val Pro Pro Arg Ser Ala
             95                 100                 105

Phe Ser Ala Lys Arg Ser Glu Ser Arg Val Pro Pro Pro Ser Asp
            110                 115                 120

Ala Pro Leu Pro Phe Asp Arg Val Leu Val Asn Glu Gln Gly His
            125                 130                 135

Tyr Asp Ala Val Thr Gly Lys Phe Thr Cys Gln Val Pro Gly Val
            140                 145                 150

Tyr Tyr Phe Ala Val His Ala Thr Val Tyr Arg Ala Ser Leu Gln
            155                 160                 165

Phe Asp Leu Val Lys Asn Gly Glu Ser Ile Ala Ser Phe Phe Gln
            170                 175                 180

Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser Gly Gly Ala
            185                 190                 195

Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln Val Gly
            200                 205                 210

Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp Ser
            215                 220                 225

Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro
            230                 235                 240

Val Phe Ala
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<210> 43
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
tacaggccca gtcaggacca gggg 24

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
agccagcctc gctctcgg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtctgcgatc aggtctgg 18

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
gaaagaggca atggattcgc 20

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
gacttacact tgccagcaca gcac 24

<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49
<211> 1876
<212> DNA
<213> Homo Sapien

<400> 49
ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50

atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100

acctgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150

gggggcatct cctggctgtg ctcctggccc tccttggcac cacctgggca 200

gaggtgtggc caccccagct gcaggagcag gctccgatgg ccggagccct 250

gaacaggaag gagagtttct tgctcctctc cctgcacaac cgcctgcgca 300

gctgggtcca gccccctgcg gctgacatgc ggaggctgga ctggagtgac 350

agcctggccc aactggctca agccagggca gccctctgtg gaatcccaac 400

cccgagcctg gcatccggcc tgtggcgcac cctgcaagtg ggctggaaca 450

tgcagctgct gcccgcgggc ttggcgtcct ttgttgaagt ggtcagccta 500

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caacgccacc tgcacccact acacgcagct cgtgtgggcc acctcaagcc 600

agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650

gcctttgtct gtgcctactc ccccggaggc aactgggagg tcaacgggaa 700

gacaatcatc ccctataaga agggtgcctg gtgttcgctc tgcacagcca 750

gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800

gtccccagga atccttgtcg catgagctgc cagaaccatg gacgtctcaa 850

catcagcacc tgccactgcc actgtccccc tggctacacg ggcagatact 900

gccaagtgag gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950

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ctgacagtga cttcgagacc aggaacttct ggatcgggct cacctacaag 1250

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ctgccatggg gtttggcaac tgcgtggagc tgcaggcttc agctgccttc 1400

aactggaacg accagcgctg caaaacccga aaccgttaca tctgccagtt 1450

tgcccaggag cacatctccc ggtggggccc agggtcctga ggcctgacca 1500

catggctccc tcgcctgccc tgggagcacc ggctctgctt acctgtctgc 1550

ccacctgtct ggaacaaggg ccaggttaag accacatgcc tcatgtccaa 1600

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gaggccagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700

gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750

acaccgccag tggtccaaaa aggctgctct cttccacctg gcccagaccc 1800

tgtggggcag cggagcttcc ctgtggcatg aaccccacgg ggtattaaat 1850

tatgaatcag ctgaaaaaaa aaaaaa 1876

<210> 50
<211> 455
<212> PRT
<213> Homo Sapien

<400> 50

Met	Leu	His	Pro	Glu	Thr	Ser	Pro	Gly	Arg	Gly	His	Leu	Leu	Ala	
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Val	Leu	Leu	Ala	Leu	Leu	Gly	Thr	Thr	Trp	Ala	Glu	Val	Trp	Pro	
				20				25						30	
Pro	Gln	Leu	Gln	Glu	Gln	Ala	Pro	Met	Ala	Gly	Ala	Leu	Asn	Arg	
				35				40						45	
Lys	Glu	Ser	Phe	Leu	Leu	Leu	Ser	Leu	His	Asn	Arg	Leu	Arg	Ser	
				50				55						60	
Trp	Val	Gln	Pro	Pro	Ala	Ala	Asp	Met	Arg	Arg	Leu	Asp	Trp	Ser	
				65				70						75	
Asp	Ser	Leu	Ala	Gln	Leu	Ala	Gln	Ala	Arg	Ala	Ala	Leu	Cys	Gly	
				80				85						90	
Ile	Pro	Thr	Pro	Ser	Leu	Ala	Ser	Gly	Leu	Trp	Arg	Thr	Leu	Gln	
				95				100						105	
Val	Gly	Trp	Asn	Met	Gln	Leu	Leu	Pro	Ala	Gly	Leu	Ala	Ser	Phe	

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                110                 115                 120

Val Glu Val Val Ser Leu Trp Phe Ala Glu Gly Gln Arg Tyr Ser
                125                 130                 135

His Ala Ala Gly Glu Cys Ala Arg Asn Ala Thr Cys Thr His Tyr
                140                 145                 150

Thr Gln Leu Val Trp Ala Thr Ser Ser Gln Leu Gly Cys Gly Arg
                155                 160                 165

His Leu Cys Ser Ala Gly Gln Thr Ala Ile Glu Ala Phe Val Cys
                170                 175                 180

Ala Tyr Ser Pro Gly Gly Asn Trp Glu Val Asn Gly Lys Thr Ile
                185                 190                 195

Ile Pro Tyr Lys Lys Gly Ala Trp Cys Ser Leu Cys Thr Ala Ser
                200                 205                 210

Val Ser Gly Cys Phe Lys Ala Trp Asp His Ala Gly Gly Leu Cys
                215                 220                 225

Glu Val Pro Arg Asn Pro Cys Arg Met Ser Cys Gln Asn His Gly
                230                 235                 240

Arg Leu Asn Ile Ser Thr Cys His Cys His Cys Pro Pro Gly Tyr
                245                 250                 255

Thr Gly Arg Tyr Cys Gln Val Arg Cys Ser Leu Gln Cys Val His
                260                 265                 270

Gly Arg Phe Arg Glu Glu Glu Cys Ser Cys Val Cys Asp Ile Gly
                275                 280                 285

Tyr Gly Gly Ala Gln Cys Ala Thr Lys Val His Phe Pro Phe His
                290                 295                 300

Thr Cys Asp Leu Arg Ile Asp Gly Asp Cys Phe Met Val Ser Ser
                305                 310                 315

Glu Ala Asp Thr Tyr Tyr Arg Ala Arg Met Lys Cys Gln Arg Lys
                320                 325                 330

Gly Gly Val Leu Ala Gln Ile Lys Ser Gln Lys Val Gln Asp Ile
                335                 340                 345

Leu Ala Phe Tyr Leu Gly Arg Leu Glu Thr Thr Asn Glu Val Thr
                350                 355                 360

Asp Ser Asp Phe Glu Thr Arg Asn Phe Trp Ile Gly Leu Thr Tyr
                365                 370                 375

Lys Thr Ala Lys Asp Ser Phe Arg Trp Ala Thr Gly Glu His Gln
                380                 385                 390

Ala Phe Thr Ser Phe Ala Phe Gly Gln Pro Asp Asn His Gly Leu
                395                 400                 405
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Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
cggacgcgtg ggctgggcgc tgcaaagcgt gtcccgccgg gtccccgagc 50

gtcccgcgcc ctcgccccgc catgctcctg ctgctggggc tgtgcctggg 100

gctgtccctg tgtgtggggt cgcaggaaga ggcgcagagc tggggccact 150

cttcggagca ggatggactc agggtcccga ggcaagtcag actgttgcag 200

aggctgaaaa ccaaaccttt gatgacagaa ttctcagtga agtctaccat 250

catttcccgt tatgccttca ctacggtttc ctgcagaatg ctgaacagag 300

cttctgaaga ccaggacatt gagttccaga tgcagattcc agctgcagct 350

ttcatcacca acttcactat gcttattgga gacaaggtgt atcagggcga 400

aattacagag agagaaaaga agagtggtga tagggtaaaa gagaaaagga 450

ataaaaccac agaagaaaat ggagagaagg ggactgaaat attcagagct 500

tctgcagtga ttcccagcaa ggacaaagcc gccttttttcc tgagttatga 550

ggagcttctg cagaggcgcc tgggcaagta cgagcacagc atcagcgtgc 600

ggccccagca gctgtccggg aggctgagcg tggacgtgaa tatcctggag 650

agcgcgggca tcgcatccct ggaggtgctg ccgcttcaca acagcaggca 700

gaggggcagt gggcgcgggg aagatgattc tgggcctccc ccatctactg 750

tcattaacca aaatgaaaca tttgccaaca taatttttaa acctactgta 800

gtacaacaag ccaggattgc ccagaatgga attttgggag actttatcat 850

tagatatgac gtcaatagag aacagagcat tggggacatc caggttctaa 900

atggctattt tgtgcactac tttgctccta aagaccttcc tcctttaccc 950

aagaatgtgg tattcgtgct tgacagcagt gcttctatgg tgggaaccaa 1000

actccggcag accaaggatg ccctcttcac aattctccat gacctccgac 1050

cccaggaccg tttcagtatc attggatttt ccaaccggat caaagtatgg 1100

aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150

gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200

tgcagagggc catcaggctc ctcaacaagt acgtggccca cagtggcatt 1250

ggagaccgga gcgtgtccct catcgtcttc ctgacggatg ggaagcccac 1300

ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350

cccgaggcca agtctgcatc ttcaccattg gcatcggcaa cgacgtggac 1400

ttcaggctgc tggagaaact gtcgctggag aactgtggcc tcacacggcg 1450

cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500

aaatcaggac cccgctcctc tctgacatcc gcatcgatta tcccccccagc 1550

tcagtggtgc aggccaccaa gaccctgttc cccaactact tcaacggctc 1600

ggagatcatc attgcgggga agctggtgga caggaagctg gatcacctgc 1650

acgtggaggt caccgccagc aacagtaaga aattcatcat cctgaagaca 1700

gatgtgcctg tgcggcctca gaaggcaggg aaagatgtca caggaagccc 1750

caggcctgga ggcgatggag agggggacac caaccacatc gagcgtctct 1800

ggagctacct caccacaaag gagctgctga gctcctggct gcaaagtgac 1850

gatgaaccgg agaaggagcg gctgcggcag cgggcccagg ccctggctgt 1900

gagctaccgc ttcctcactc ccttcacctc catgaagctg agggggccgg 1950

tcccacgcat ggatggcctg gaggaggccc acggcatgtc ggctgccatg 2000

ggacccgaac cggtggtgca gagcgtgcga ggagctggca cgcagccagg 2050

acctttgctc aagaagccaa actccgtcaa aaaaaaacaa aacaaaacaa 2100

aaaaaagaca tgggagagat ggtgtttttc ctctccacca cctggggata 2150

cgatgagaag atggccacct gcaagccagg aagacggccc tcaccagaca 2200

ccatgtctgc tggcaccttg atcttggacc tcccagcctc cagaactgtg 2250

agaaataaat gtgttttgtt taagctaaaa aaaaaaaaaa aaaaaaaaaa 2300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2331

<210> 55
<211> 694
<212> PRT
<213> Homo Sapien

<400> 55

Met	Leu	Leu	Leu	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Ser	Leu	Cys	Val	
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Gly	Ser	Gln	Glu	Glu	Ala	Gln	Ser	Trp	Gly	His	Ser	Ser	Glu	Gln	
				20				25						30	
Asp	Gly	Leu	Arg	Val	Pro	Arg	Gln	Val	Arg	Leu	Leu	Gln	Arg	Leu	
				35				40						45	
Lys	Thr	Lys	Pro	Leu	Met	Thr	Glu	Phe	Ser	Val	Lys	Ser	Thr	Ile	
				50				55						60	
Ile	Ser	Arg	Tyr	Ala	Phe	Thr	Thr	Val	Ser	Cys	Arg	Met	Leu	Asn	
				65				70						75	
Arg	Ala	Ser	Glu	Asp	Gln	Asp	Ile	Glu	Phe	Gln	Met	Gln	Ile	Pro	
				80				85						90	
Ala	Ala	Ala	Phe	Ile	Thr	Asn	Phe	Thr	Met	Leu	Ile	Gly	Asp	Lys	
				95				100						105	
Val	Tyr	Gln	Gly	Glu	Ile	Thr	Glu	Arg	Glu	Lys	Lys	Ser	Gly	Asp	
				110				115						120	

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu
125 130 135

Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys
140 145 150

Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg
155 160 165

Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln
170 175 180

Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala
185 190 195

Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln
200 205 210

Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser
215 220 225

Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys
230 235 240

Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu
245 250 255

Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile
260 265 270

Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala
275 280 285

Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu
290 295 300

Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys
305 310 315

Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg
320 325 330

Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp
335 340 345

His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val
350 355 360

Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly
365 370 375

Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His
380 385 390

Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr
395 400 405

Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu

410 415 420

Asn Asn Thr Arg Glu Ala Ala Arg Gly Gln Val Cys Ile Phe Thr
425 430 435

Ile Gly Ile Gly Asn Asp Val Asp Phe Arg Leu Leu Glu Lys Leu
440 445 450

Ser Leu Glu Asn Cys Gly Leu Thr Arg Arg Val His Glu Glu Glu
455 460 465

Asp Ala Gly Ser Gln Leu Ile Gly Phe Tyr Asp Glu Ile Arg Thr
470 475 480

Pro Leu Leu Ser Asp Ile Arg Ile Asp Tyr Pro Pro Ser Ser Val
485 490 495

Val Gln Ala Thr Lys Thr Leu Phe Pro Asn Tyr Phe Asn Gly Ser
500 505 510

Glu Ile Ile Ile Ala Gly Lys Leu Val Asp Arg Lys Leu Asp His
515 520 525

Leu His Val Glu Val Thr Ala Ser Asn Ser Lys Lys Phe Ile Ile
530 535 540

Leu Lys Thr Asp Val Pro Val Arg Pro Gln Lys Ala Gly Lys Asp
545 550 555

Val Thr Gly Ser Pro Arg Pro Gly Gly Asp Gly Glu Gly Asp Thr
560 565 570

Asn His Ile Glu Arg Leu Trp Ser Tyr Leu Thr Thr Lys Glu Leu
575 580 585

Leu Ser Ser Trp Leu Gln Ser Asp Asp Glu Pro Glu Lys Glu Arg
590 595 600

Leu Arg Gln Arg Ala Gln Ala Leu Ala Val Ser Tyr Arg Phe Leu
605 610 615

Thr Pro Phe Thr Ser Met Lys Leu Arg Gly Pro Val Pro Arg Met
620 625 630

Asp Gly Leu Glu Glu Ala His Gly Met Ser Ala Ala Met Gly Pro
635 640 645

Glu Pro Val Val Gln Ser Val Arg Gly Ala Gly Thr Gln Pro Gly
650 655 660

Pro Leu Leu Lys Lys Pro Asn Ser Val Lys Lys Lys Gln Asn Lys
665 670 675

Thr Lys Lys Arg His Gly Arg Asp Gly Val Phe Pro Leu His His
680 685 690

Leu Gly Ile Arg

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatatc agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg gggtgcccga catggcgagt gtagtgctgc cgagcggatc 50

ccagtgtgcg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100

tgctgttgct cttctccgcc gcggcactga tccccacagg tgatgggcag 150

aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgaccat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250

ccaacaggca gaccatttat ttcagggact tcaggccttt gaaggacagc 300

aggtttcagt tgctgaattt ttctagcagt gaactcaaag tatcattgac 350

aaacgtctca atttctgatg aaggaagata cttttgccag ctctataccg 400

atcccccaca ggaaagttac accaccatca cagtcctggt cccaccacgt 450

aatctgatga tcgatatcca gaaagacact gcggtggaag gtgaggagat 500

tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550

ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600

tcagacatgt acactgtgac cagtcagctg atgctgaagg tgcacaagga 650

ggacgatggg gtcccagtga tctgccaggt ggagcaccct gcggtcactg 700

gaaacctgca gacccagcgg tatctagaag tacagtataa gcctcaagtg 750

cacattcaga tgacttatcc tctacaaggc ttaacccggg aaggggacgc 800

gcttgagtta acatgtgaag ccatcgggaa gccccagcct gtgatggtaa 850

cttgggtgag agtcgatgat gaaatgcctc aacacgccgt actgtctggg 900

cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataccg 950

ctgtgaagct tcaaacatag tggggaaagc tcactcggat tatatgctgt 1000

atgtatacga tccccccaca actatccctc ctcccacaac aaccaccacc 1050

accaccacca ccaccaccac caccatcctt accatcatca cagattcccg 1100

agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcggtg 1150

gcgtcgtggc ggtggtggtg ttcgccatgc tgtgcttgct catcattctg 1200

gggcgctatt ttgccagaca taaaggtaca tacttcactc atgaagccaa 1250

aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300

gaggacagaa caactccgaa gaaaagaaag agtacttcat ctagatcagc 1350

ctttttgttt caatgaggtg tccaactggc cctatttaga tgataaagag 1400

acagtgatat tgg 1413

<210> 61
<211> 440
<212> PRT
<213> Homo Sapien

<400> 61
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

Ala Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Leu Leu Leu Leu
20 25 30

Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu
35 40 45

Phe Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile
50 55 60

Ser Cys Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu
65 70 75

Asn Pro Asn Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu
80 85 90

Lys Asp Ser Arg Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu
95 100 105

Lys Val Ser Leu Thr Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr
110 115 120

Phe Cys Gln Leu Tyr Thr Asp Pro Pro Gln Glu Ser Tyr Thr Thr
125 130 135

Ile Thr Val Leu Val Pro Pro Arg Asn Leu Met Ile Asp Ile Gln
140 145 150

Lys Asp Thr Ala Val Glu Gly Glu Glu Ile Glu Val Asn Cys Thr
155 160 165

Ala Met Ala Ser Lys Pro Ala Thr Thr Ile Arg Trp Phe Lys Gly
170 175 180

Asn Thr Glu Leu Lys Gly Lys Ser Glu Val Glu Glu Trp Ser Asp
185 190 195

Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys Val His Lys Glu
200 205 210

Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His Pro Ala Val
215 220 225

Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln Tyr Lys
230 235 240

Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu Thr
245 250 255

Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
260 265 270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met
275 280 285

Pro Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn
290 295 300

Leu Asn Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn

305 310 315

Ile Val Gly Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp
320 325 330

Pro Pro Thr Thr Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr
335 340 345

Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg
350 355 360

Ala Gly Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile
365 370 375

Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu
380 385 390

Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe
395 400 405

Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr
410 415 420

Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn Asn Ser Glu Glu Lys
425 430 435

Lys Glu Tyr Phe Ile
440

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 62
ggcttctgct gttgctcttc tccg 24

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 63
gtacactgtg accagtcagc 20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcgggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50

cctcgggccc gacccgccag gaaagactga ggccgcggcc tgccccgccc 100

ggctccctgc gccgccgccg cctcccggga cagaagatgt gctccagggt 150

ccctctgctg ctgccgctgc tcctgctact ggccctgggg cctggggtgc 200

agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250

actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggt 300

ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350

ttgccggcct gccgggcctg cagctcctgg acctgtcaca gaaccagatc 400

gccagcctgc gcctgccccg cctgctgctg ctggacctca gccacaacag 450

cctcctggcc ctggagcccg gcatcctgga cactgccaac gtggaggcgc 500

tgcggctggc tggtctgggg ctgcagcagc tggacgaggg gctcttcagc 550

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cgcgagagcc acgtcacact ggccagccct gaggagacgc gctgccactt 900

cccgcccaag aacgctggcc ggctgctcct ggagcttgac tacgccgact 950

ttggctgccc agccaccacc accacagcca cagtgcccac cacgaggccc 1000

gtggtgcggg agcccacagc cttgtcttct agcttggctc ctacctggct 1050

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gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2300

gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttggc 2350

cccaggaagc gaaggaacaa aagaaactgg aaaggaagat gctttaggaa 2400

catgttttgc ttttttaaaa tatatatata tttataagag atcctttccc 2450

atttattctg ggaagatgtt tttcaaactc agagacaagg actttggttt 2500

ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa aaataaaaaa 2550

aaaaa 2555

<210> 69
<211> 598
<212> PRT
<213> Homo Sapien

<400> 69

Met	Cys	Ser	Arg	Val	Pro	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	
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Ala	Leu	Gly	Pro	Gly	Val	Gln	Gly	Cys	Pro	Ser	Gly	Cys	Gln	Cys	
				20					25						30
Ser	Gln	Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr	
				35					40						45
Val	Pro	Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe	
				50					55						60
Glu	Asn	Gly	Ile	Thr	Met	Leu	Asp	Ala	Ser	Ser	Phe	Ala	Gly	Leu	
				65					70						75
Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser	
				80					85						90
Leu	Arg	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Asp	Leu	Ser	His	Asn	Ser	
				95					100						105
Leu	Leu	Ala	Leu	Glu	Pro	Gly	Ile	Leu	Asp	Thr	Ala	Asn	Val	Glu	

110 115 120

Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly
125 130 135

Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp
140 145 150

Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly
155 160 165

Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu
170 175 180

Arg Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp
185 190 195

Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly
200 205 210

Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe
215 220 225

Asn Cys Val Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu
230 235 240

Ser His Val Thr Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe
245 250 255

Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala
260 265 270

Asp Phe Gly Cys Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr
275 280 285

Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu
290 295 300

Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro
305 310 315

Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln
320 325 330

Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys
335 340 345

His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly
350 355 360

Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg
365 370 375

Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr
380 385 390

Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu
395 400 405

Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg
410 415 420

Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr
425 430 435

Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu
440 445 450

Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro
455 460 465

Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr
470 475 480

Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg
485 490 495

Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val
500 505 510

Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg
515 520 525

Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val
530 535 540

Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro
545 550 555

Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu
560 565 570

Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly
575 580 585

Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile
590 595

<210> 70
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ccctccactg ccccaccgac tg 22

<210> 71
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccaccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgccc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt cccttctgca ccactgcccg tacccttacc 50

cgccccgcca cctccttgct accccactct tgaaaccaca gctgttggca 100

gggtccccag ctcatgccag cctcatctcc tttcttgcta gcccccaaag 150

ggcctccagg caacatgggg ggcccagtca gagagccggc actctcagtt 200

gccctctggt tgagttgggg ggcagctctg ggggccgtgg cttgtgccat 250

ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300

gccggctgca ggggacagga ggcccctccc agaatgggga agggtatccc 350

tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

tggggagaga tcccggaaaa ggagagcagt gctcacccaa aaacagaaga 450

agcagcactc tgtcctgcac ctggttccca ttaacgccac ctccaaggat 500

gactccgatg tgacagaggt gatgtggcaa ccagctctta ggcgtgggag 550

aggcctacag gcccaaggat atggtgtccg aatccaggat gctggagttt 600

atctgctgta tagccaggtc ctgtttcaag acgtgacttt caccatgggt 650

caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700

tataagaagt atgccctccc acccggaccg ggcctacaac agctgctata 750

gcgcaggtgt cttccattta caccaagggg atattctgag tgtcataatt 800

ccccgggcaa gggcgaaact taacctctct ccacatggaa ccttcctggg 850

gtttgtgaaa ctgtgattgt gttataaaaa gtggctccca gcttggaaga 900

ccagggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950

agggaatgtg caggaacaga ggcatcttcc tgggtttggc tccccgttcc 1000

tcacttttcc cttttcattc ccacccccta gactttgatt ttacggatat 1050

cttgcttctg ttccccatgg agctccg 1077

<210> 76
<211> 250
<212> PRT
<213> Homo Sapien

<400> 76

Met	Pro	Ala	Ser	Ser	Pro	Phe	Leu	Leu	Ala	Pro	Lys	Gly	Pro	Pro	
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				20				25						30	
Leu	Trp	Leu	Ser	Trp	Gly	Ala	Ala	Leu	Gly	Ala	Val	Ala	Cys	Ala	
				35				40						45	
Met	Ala	Leu	Leu	Thr	Gln	Gln	Thr	Glu	Leu	Gln	Ser	Leu	Arg	Arg	
				50				55						60	
Glu	Val	Ser	Arg	Leu	Gln	Gly	Thr	Gly	Gly	Pro	Ser	Gln	Asn	Gly	
				65				70						75	
Glu	Gly	Tyr	Pro	Trp	Gln	Ser	Leu	Pro	Glu	Gln	Ser	Ser	Asp	Ala	
				80				85						90	
Leu	Glu	Ala	Trp	Glu	Asn	Gly	Glu	Arg	Ser	Arg	Lys	Arg	Arg	Ala	
				95				100						105	
Val	Leu	Thr	Gln	Lys	Gln	Lys	Lys	Gln	His	Ser	Val	Leu	His	Leu	
				110				115						120	

Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu
125 130 135

Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala
140 145 150

Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu
155 160 165

Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln
170 175 180

Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg
185 190 195

Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser
200 205 210

Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
215 220 225

Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
245 250

<210> 77
<211> 2849
<212> DNA
<213> Homo Sapien

<400> 77
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ggtcgcagag acctcggaga ccgcgccggg gagacggagg tgctgtgggt 100

gggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150

tgccgtcctc cggaagacct ttcccctgc tctgtttcct tcaccgagtc 200

tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250

ctctaggggc ggcgcgggag gagcggccgg cgggacggag ggcccggcag 300

gaagatgggc tcccgtggac agggactctt gctggcgtac tgcctgctcc 350

ttgcctttgc ctctggcctg gtcctgagtc gtgtgcccca tgtccagggg 400

gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450

tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500

aggggctccc tgcttcccgg tgcttgcgct gctgtgaccc cggtacctcc 550

atgtacccgg cgaccgccgt gccccagatc aacatcacta tcttgaaagg 600

ggagaagggt gaccgcggag atcgaggcct ccaagggaaa tatggcaaaa 650

caggctcagc aggggccagg ggccacactg gacccaaagg gcagaagggc 700

tccatggggg cccctgggga gcggtgcaag agccactacg ccgccttttc 750

ggtgggccgg aagaagccca tgcacagcaa ccactactac cagacggtga 800

tcttcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850

ggcaagttct actgctacgt gcccggcctc tacttcttca gcctcaacgt 900

gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950

aggaggtggt gatcttgttc gcgcaggtgg gcgaccgcag catcatgcaa 1000

agccagagcc tgatgctgga gctgcgagag caggaccagg tgtgggtacg 1050

cctctacaag ggcgaacgtg agaacgccat cttcagcgag gagctggaca 1100

cctacatcac cttcagtggc tacctggtca agcacgccac cgagccctag 1150

ctggccggcc acctcctttc ctctcgccac cttccacccc tgcgctgtgc 1200

tgaccccacc gcctcttccc cgatccctgg actccgactc cctggctttg 1250

gcattcagtg agacgccctg cacacacaga aagccaaagc gatcggtgct 1300

cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350

ggcggggcac ccgcgagaac cctctgggac cttccgcggc cctctctgca 1400

cacatcctca agtgaccccg cacggcgaga cgcgggtggc ggcagggcgt 1450

cccagggtgc ggcaccgcgg ctccagtcct tggaaataat taggcaaatt 1500

ctaaaggtct caaaaggagc aaagtaaacc gtggaggaca aagaaaaggg 1550

ttgttatttt tgtctttcca gccagcctgc tggctcccaa gagagaggcc 1600

ttttcagttg agactctgct taagagaaga tccaaagtta aagctctggg 1650

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agccacgtag gaactttctt gagggatagg tggaccctga catccctgtg 1750

gccttgccca agggctctgc tggtctttct gagtcacagc tgcgaggtga 1800

tgggggctgg ggccccaggc gtcagcctcc cagagggaca gctgagcccc 1850

ctgccttggc tccaggttgg tagaagcagc cgaagggctc ctgacagtgg 1900

ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgaggggcag 1950

agctccttgg tacatccatg tgtggctctg ctccaccccc gtgccacccc 2000

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ggcccccaaa cccccgctgc ctctcttcct tccccccatc ccccacctgg 2650

ttttgactaa tcctgcttcc ctctctgggc ctggctgccg ggatctgggg 2700

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gagttgctgt gggcgtgccc ggaagcagag cgccacactc gctgcttaag 2800

ctccccccagc tctttccaga aaacattaaa ctcagaattg tgttttcaa 2849

<210> 78
<211> 281
<212> PRT
<213> Homo Sapien

<400> 78
Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
1 5 10 15

Leu Ala Phe Ala Ser Gly Leu Val Leu Ser Arg Val Pro His Val
20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110 115 120

Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly
125 130 135

Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val
140 145 150

Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val
155 160 165

Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met
170 175 180

Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe
185 190 195

Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His
200 205 210

Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val
215 220 225

Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu
230 235 240

Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg
245 250 255

Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe
260 265 270

Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro
275 280

<210> 79
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
tacaggccca gtcaggacca gggg 24

<210> 80
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctgaagaagt agaggccggg cacg 24

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccggtgctt gcgctgctgt gaccccggta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gcggagcatc cgctgcggtc ctcgccgaga cccccgcgcg gattcgccgg 50

tccttcccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100

ggcgccgggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150

cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200

gaccaaaact aaactgaaat ttaaaatgtt cttcggggga gaagggagct 250

tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300

agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350

gtcatctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400

ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450

gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500

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tttggatcct cagatcacct ggagaaacta tttaagatgg atgaagcaag 800

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tatgtcaaat gtggagtctt ccactatgaa taaaactgct tcctgggaag 1300

gtagggaggc cagtccaggc agttcctccc agggcagtgt tccagaaaat 1350

cagtacggcc ttccatttga aaaatggctt cttatcgggt ccctgctctt 1400

tggtgtcctg ttcctggtga taggcctcgt cctcctgggt agaatccttt 1450

cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500

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ttttttttt ggagacagag tcttgctctg ttgcccaggc tggagtgcag 1700

tagcacgatc tcggctctca ccgcaacctc cgtctcctgg gttcaagcga 1750

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acacctgggt gatttttgta tttttagtag agacggggtt tcaccatgtt 1850

ggtcaggctg gtctcaaact cctgacctag tgatccaccc tcctcggcct 1900

cccaaagtgc tgggattaca ggcatgagcc accacagctg gccccttct 1950

gttttatgtt tggtttttga gaaggaatga agtgggaacc aaattaggta 2000

attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050

aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100

tatgcaaaga aacaggttag gacatctagg ttccaattca ttcacattct 2150

tggttccaga taaaatcaac tgtttatatc aatttctaat ggatttgctt 2200

ttctttttat atggattcct ttaaaactta ttccagatgt agttccttcc 2250

aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 83
<211> 431
<212> PRT
<213> Homo Sapien

<400> 83
Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile
1 5 10 15

Ile Cys Phe Leu Thr Leu Arg Leu Ser Ala Ser Gln Asn Cys Leu
20 25 30

Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
35 40 45

Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
50 55 60

Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
65 70 75

Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
80 85 90

Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
95 100 105

Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
110 115 120

Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
125 130 135

Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
140 145 150

Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
155 160 165

Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
170 175 180

His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
185 190 195

Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser
200 205 210

Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala
215 220 225

Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
230 235 240

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr
245 250 255

Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro
260 265 270

Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr
275 280 285

Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr
290 295 300

Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly

305 310 315

Ser Leu Glu Thr Ile Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu
320 325 330

Asn Thr Gly Asn Val Tyr Asn Pro Thr Ala Leu Ser Met Ser Asn
335 340 345

Val Glu Ser Ser Thr Met Asn Lys Thr Ala Ser Trp Glu Gly Arg
350 355 360

Glu Ala Ser Pro Gly Ser Ser Ser Gln Gly Ser Val Pro Glu Asn
365 370 375

Gln Tyr Gly Leu Pro Phe Glu Lys Trp Leu Leu Ile Gly Ser Leu
380 385 390

Leu Phe Gly Val Leu Phe Leu Val Ile Gly Leu Val Leu Leu Gly
395 400 405

Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg Tyr Ser Arg Leu
410 415 420

Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
425 430

<210> 84
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 84
agggaggatt atccttgacc tttgaagacc 30

<210> 85
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 85
gaagcaagtg cccagctc 18

<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
cgggtccctg ctctttgg 18

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
caccgtagct gggagcgcac tcac 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
agtgtaagtc aagctccc 18

<210> 89
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
gcttcctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

<210> 90
<211> 957
<212> DNA
<213> Homo Sapien

<400> 90
cctggaagat gcgcccattg gctggtggcc tgctcaaggt ggtgttcgtg 50

gtcttcgcct ccttgtgtgc ctggtattcg gggtacctgc tcgcagagct 100

cattccagat gcacccctgt ccagtgctgc ctatagcatc cgcagcatcg 150

gggagaggcc tgtcctcaaa gctccagtcc ccaaaaggca aaaatgtgac 200

cactggactc cctgcccatc tgacacctat gcctacaggt tactcagcgg 250

aggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacctactta 300

tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350

aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400

aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450

aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

aacgatgcca agaatgccat agaagcactt ggaagtaaag aaatcaggaa 550

catgaaattc aggtctagct gggtatttat tgcagcaaaa ggcttggaac 600

tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650

aacagatatt ctggctggcc tgcagagatc cagatagaag gctgcatacc 700

caaagaacga agctgacact gcagggtcct gagtaaatgt gttctgtata 750

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gcccatattt gatgagtatt ttgggtttgt tgtaaaccaa tgaacatttg 850

ctagttgtat caaatcttgg tacgcagtat ttttatacca gtatttatg 900

tagtgaagat gtcaattagc aggaaactaa aatgaatgga aattcttaaa 950

aaaaaaa 957

<210> 91
<211> 235
<212> PRT
<213> Homo Sapien

<400> 91
Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
1 5 10 15

Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
20 25 30

Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
35 40 45

Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
50 55 60

Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
65 70 75

Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
80 85 90

Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
95 100 105

Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
110 115 120

Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
125 130 135

Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
140 145 150

Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
200 205 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
215 220 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
230 235

<210> 92
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
aatgtgacca ctggactccc 20

<210> 93
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
aggcttggaa ctcccttc 18

<210> 94
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
aagattcttg agcgattcca gctg 24

<210> 95
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
aatccctgct cttcatggtg acctatgacg acggaagcac aagactg 47

<210> 96
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
ctcaagaagc acgcgtactg c 21

<210> 97
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
ccaacctcag cttccgcctc tacga 25

<210> 98
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
catccaggct cgccactg 18

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 99
tggcaaggaa tgggaacagt 20

<210> 100
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 100
atgctgccag acctgatcgc agaca 25

<210> 101
<211> 19
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